

	AUTHORS	Yan,M., Wang,L.C., Hymowitz,S.G., Schilbach,S., Lee,J., Goddard,A., de Vos,A.M., Gao,W.Q. and Dixit,V.M.
	TITLE	Two-amino acid molecular switch in an epithelial morphogen that regulates binding to two distinct receptors
	JOURNAL	Science 290 (5491), 523-527 (2000)
	PUBLMED	11039935
	REFERENCE	2 (bases 1 to 894)
BASE COUNT	255	a 327 c 314 g 266 t
ORIGIN		
Query Match	88 2%	Score 611 4; DB 6; Length 1162;
Best Local Similarity	99.0%	Pred. No. 4.4e-167; Mismatches 6; Indels 0; Gaps 0;
Matches	615;	Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy	1 ATGGATGCGCAAGAAATGGTACTGGGACCAATTGGGACGGTGACCTGCCAACGG	60
Db	104 ATGGATGCGCAAGAAATGGTACTGGGACGGTGACCTGCCAACGG	163
Qy	61 TGTGTCCTGACAGAGGATCCAGGATGTTATGGAGGGTGAGATGCCAACGG	120
Db	164 TGTGTCCTGACAGAGGATCCAGGATGTTATGGAGGGTGAGATGCCAACGG	223
Qy	121 TGCACAGCCCTCTCCAGGACAAAGCAGCTGGGCCACACAAATGCGAGCT	180
Db	224 TGCACAGCCCTCTCCAGGACAAAGCAGCTGGGCCACACAAATGCGAGCT	283
Qy	181 TGCATCAGCTCTGCTCATCAATGGTGTCAAGAGGTCACAGCTACCTTAAT	240
Db	284 TGCATCAGCTCTGCTCATCAATGGTGTCAAGAGGTCACAGCTACCTTAAT	343
Qy	241 GCTGTCCTGGGGACTGTTGCCAGGTCTACCGAAGACACGATGGAGCTGCAG	300
Db	344 GCTGTCCTGGGGACTGTTGCCAGGTCTACCGAAGACACGATGGAGCTGCAG	403
Qy	301 GACAGAGTCATCCGTCACCGAGCACCCACCTCTGGATCATGGCCTTC	360
Db	404 GACAAAGAGTCATCCGTCACCGAGCACCCACCTCTGGATCATGGCCTTC	463
Qy	361 CAGTGGAGCTAGGGAGGAGATGCCACCCAGTGAGGTCTTC	420
Db	464 CAGTGGAGCTAGGGAGGAGATGCCACCCAGTGAGGTCTTC	523
Qy	421 GCAGTCGTGAGCAGCCGTCTAGTGGTTACCCCTCGCTCTCTCTCTC	480
Db	524 GCAGTCGTGAGCAGCCGTCTAGTGGTTACCCCTCGCTCTCTCTC	583
Qy	481 TACTGAAAGCTCTCAACAGACATGCCAGGGTGGAGGTTCTGAGTTAGGT	540
Db	584 TACTGCAAGCTCTCAACAGACATGCCAGGGTGGAGGTTCTGAGTTAGGT	643
Qy	541 GATAAACAGAAAGAGGAATCTCTCCGGCCACCCAGGAGGACAGTGT	600
Db	644 GATAAACAGAAAGAGGAATCTCTCCGGCCACCCAGGAGGACAGTGT	703
RESULT 2		
AP298812 LOCUS	A2F298812	894 bp mRNA linear PRI 01-NOV-2000
DEFINITION	Homo sapiens X-linked ectodysplasin-A2 receptor (XEDAR) mRNA, complete cds.	
ACCESSION	AF298812	
VERSION	AF298812.1	GI:11066914
KEYWORDS	human.	
ORGANISM	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 894)	

Db 481 TACTGCAAGCAGTCTTCACAGACATGCCAGGGTTGCTGAGTTGAGCT 540
 Qy 541 GATAAACACGCCAAGGAGGATCTCTCTCCCTGCCACCCAGCAAGGACAGCT 600
 Db 541 GATAAACACGCCAAGGAGGATCTCTCTCCCTGCCACCCAGCAAGGACAGCT 600
 Qy 601 GASTGCCAAGT 611
 Db 601 GAGTCCCCAAGT 611

RESULT 3
 AX127563
 LOCUS AX127563 Sequence 28 from Patent WO0130850. DNA linear PAT 15-MAY-2001
 DEFINITION AX127563.1 GI:14134260
 VERSION AX127563
 KEYWORDS SOURCE
 ORGANISM synthetic construct.
 REFERENCE
 AUTHORS Xu, W., Lofton-Day, C.E., Henne, R., Yao, Y., Novak, J.E., Foster, D.C.
 TITLE Unlr polypeptides
 JOURNAL Patent: WO 0130850-A 28 03-MAY-2001;
 ZymoGenetics, Inc. (US)
 FEATURES Location/O qualifiers
 source 1. .891
 /organism="synthetic construct"
 /db_xref="txon:32630"
 /note="degenerate sequence"
 misc_feature 1. .891
 BASE COUNT 141 a 105 c 150 g 112 t 383 others
 ORIGIN
 Query Match 64.4%; Score 446.6; DB 6; Length 891;
 Best Local Similarity 58.6%; Pred. No. 4_5e-119;
 Matches 360; Conservative 147; Mismatches 107; Indels 0; Gaps 0;
 Qy 1 ATGGATGCCAAGAAATGAGTACTGGGACCAAGGGGACGGGTGTCACCTCCAACGG 60
 Db 1 ATGGATGCCAAGAAATGAGTACTGGGACCAAGGGGACGGGTGTCACCTCCAACGG 60
 Qy 61 TGGTGTCTGGAGGACTCTATCCAAAGATTCTGGTATGGAGGGGGAGATGCTAC 120
 Db 61 TGGTGTCTGGAGGACTCTATCCAAAGATTCTGGTATGGAGGGGGAGATGCTAC 120
 Qy 121 TGCACAGCCTGCCCTCGCGGTACRAAAGCAGCTGGGCCACCAAAATGTCAGT 180
 Db 121 TGCACAGCCTGCCCTCGCGGTACRAAAGCAGCTGGGCCACCAAAATGTCAGT 180
 Qy 181 TGGCATCACCTGTCTGTCTCATCATCGTGTGAGGTCACCTGCACGTCTCTTA 240
 Db 181 TGGTGTCTGGAGGACTCTATCCAAAGACAGCAGCTGGAGGCCCTGCAG 300
 Qy 241 GCGTGTCTGGAGGACTCTATCCAAAGACAGCAGCTGGAGGCCCTGCAG 300
 Db 241 GCGTGTCTGGAGGACTCTATCCAAAGACAGCAGCTGGAGGCCCTGCAG 300
 Qy 301 GGCAAGAGTCATCCCGTGCAGGAAGCAGACCCCACTCTGGGTCAATGTGCCTC 360
 Db 301 GAYCARGARTGYATHCCNTGYACNAARCARACACNCACNWNNGARGTNC 360
 Qy 361 CAGTGTGACTTGAGGAGCAATGCCACAGTGTGCCCTCTAGGGCCACACTGT 420
 Db 361 GAYCARTGYATHCCNTGYACNAARCARACACNCACNWNNGARGTNC 420
 Qy 421 GCAGTGGGAGGAGCCCTGCTAGTGGGTGTTACCTGGCTCTCTGGGCTCTCTC 480
 Db 421 GCGTGTCTGGAGGACTCTATCCAAAGACAGCAGCTGGAGGCCCTGCAG 480

RESULT 4
 AX127538
 LOCUS AX127538 Sequence 3 from Patent WO0130850. DNA linear PAT 15-MAY-2001
 DEFINITION AX127538.1 GI:14134243
 VERSION AX127538
 KEYWORDS SOURCE
 ORGANISM synthetic construct.
 REFERENCE
 AUTHORS Xu, W., Lofton-Day, C.E., Henne, R., Yao, Y., Novak, J.E., Foster, D.C.
 TITLE Unlr polypeptides
 JOURNAL Patent: WO 0130850-A 3 03-MAY-2001;
 ZymoGenetics, Inc. (US)
 FEATURES Location/O qualifiers
 source 1. .807
 /organism="synthetic construct"
 /db_xref="txon:32630"
 /note="degenerate sequence"
 misc_feature 1. .807
 BASE COUNT 125 a 93 c 142 g 102 t 345 others
 ORIGIN
 Query Match 64.4%; Score 446.4; DB 6; Length 807;
 Best Local Similarity 55.4%; Pred. No. 5_1e-119;
 Matches 370; Conservative 156; Mismatches 142; Indels 0; Gaps 0;
 Qy 1 ATGGATGCCAAGAAATGAGTACTGGGACCAAGGGGACGGGTGTCACCTCCAACGG 60
 Db 1 ATGGATGCCAAGAAATGAGTACTGGGACCAAGGGGACGGGTGTCACCTCCAACGG 60
 Qy 61 TGGTGTCTGGAGGACTCTATCCAAAGATTCTGGTATGGAGGGGGAGATGCTAC 120
 Db 61 TGGTGTCTGGAGGACTCTATCCAAAGATTCTGGTATGGAGGGGGAGATGCTAC 120
 Qy 121 TGCACAGCCTGCCCTCGCGGTACRAAAGCAGCTGGGCCACCAAAATGTCAGT 180
 Db 121 TGCACAGCCTGCCCTCGCGGTACRAAAGCAGCTGGGCCACCAAAATGTCAGT 180
 Qy 181 TGGCATCACCTGTCTGTCTCATCATCGTGTGAGGTCACCTGCACGTCTCTTA 240
 Db 181 TGGTGTCTGGAGGACTCTATCCAAAGACAGCAGCTGGAGGCCCTGCAG 300
 Qy 241 GCGTGTCTGGAGGACTCTATCCAAAGACAGCAGCTGGAGGCCCTGCAG 300
 Db 241 GCGTGTCTGGAGGACTCTATCCAAAGACAGCAGCTGGAGGCCCTGCAG 300
 Qy 301 GCGCAAGAGTCATCCCGTGCAGGAAGCAGACCCCACTCTGGGTCAATGTGCCTC 360
 Db 301 GAYCARGARTGYATHCCNTGYACNAARCARACACNCACNWNNGARGTNC 360
 Qy 361 CAGTGTGACTTGAGGAGCAATGCCACAGTGTGCCCTCTAGGGCCACACTGT 420
 Db 361 GAYCARTGYATHCCNTGYACNAARCARACACNCACNWNNGARGTNC 420
 Qy 421 GCAGTGGGAGGAGCCCTGCTAGTGGGTGTTACCTGGCTCTCTGGGCTCTCTC 480
 Db 421 GCGTGTCTGGAGGACTCTATCCAAAGACAGCAGCTGGAGGCCCTGCAG 480

JOURNAL	Patent: WO 0130850-A 22 03-MAY-2001;
ZymoGenetics, Inc. (US)	Location/Qualifiers
source	/organism="synthetic construct" /db_xref="taxon;32630"
BASE COUNT	290 a /note="construct" 358 c 330 g 222 t ORIGIN
Query Match	55.7%; Score 393.2; DB 6; Length 1200;
Best Local Similarity	93.2%; Pred. No. 1.7e-103;
Matches	395; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	4 GATGCCAGAAATTGAGTACTGGACCAATGGGACGGTGTGACCTGGCCAAAGGG 60
Db	109 GATGCCAGAAATTGAGTACTGGACCAATGGGACGGTGTGACCTGGCCAAAGGG 63
Qy	61 TGTGCTCTGACAGGAGCTATCCAAAGGATTCAGGATGGGACGGTGTGACCTGGCCAAAGGG 120
Db	61 TGYGCNCNCGNCARGARTINWSNHBARGATG-TGNTAIGGNGARGGGNGAYCARN 60
Qy	121 TGCACAGCTGCCCCTCTCGCAGGTACAAAGCAGCTGGGGCACCCACAATGTAGAGTG 120
Db	121 TGYACNGCNCGNCNCGNCNMGNTAYARWSNNNTGGNGAYCAYAARTGTYCARN 180
Qy	124 ACAGCTGCCCTCTCGCAGGTACAAAGCAGCTGGGGCACCCACAATGTAGAGTG 183
Db	229 ACAGCTGCCCTCTCGCAGGTACAAAGCAGCTGGGGCACCCACAATGTAGAGTG 123
Qy	169 GGTCTCTGGACAGGAGCTATCCAAAGGATTCAGGATGGGACGGTGTGACCTGGCCAAAGGG 228
Db	184 ATGACCTGTGCTGTCATCAATCGTGTGAGAGGTCAACTGCGACAGTCACTCTAATGCT 243
Qy	184 ATGACCTGTGCTGTCATCAATCGTGTGAGAGGTCAACTGCGACAGTCACTCTAATGCT 288
Db	289 ATGACCTGTGCTGTCATCAATCGTGTGAGAGGTCAACTGCGACAGTCACTCTAATGCT 348
Qy	244 GTCTGCTGGGAGCTGTTGCCAGTTCACCGAACGACGATGGGCTGAGGCTGAGGAC 303
Db	349 GTCTGCTGGGAGCTGTTGCCAGTTCACCGAACGACGATGGGCTGAGGCTGAGGAC 408
Qy	304 CAAGAGTCATCCGTCAGCAGCAGACCCACCTCTGAGCTTAATGTCCTCCAG 363
Db	409 CAAGAGTCATCCGTCAGCAGCAGACCCACCTCTGAGCTTAATGTCCTCCAG 468
Qy	364 TTGAGCTTAGGGAGCATGGACCACAGTGGCTCC 401
Db	469 TTGAGCTTAGGGAGCATGGACCACAGTGGCTCC 506
RESULT 8	
AXI27565	AXI27565 801 bp DNA linear PAT 15-MAY-2001
LOCUS	Sequence 30 from Patent WO0130850.
DEFINITION	
ACCESSION	AXI27565
VERSION	AXI27565.1 GI:14134261
KEYWORDS	
SOURCE	
ORGANISM	synthetic construct.
REFERENCE	artificial sequence.
AUTHORS	Xu,W., Lofton-Day,C.E., Henne,R., Yao,Y., Novak,J.E., Foster,D.C.
TITLE	Sequence 39 from Patent WO0130850.
DEFINITION	Sequence 39 from Patent WO0130850.
ACCESSION	AXI27574
VERSION	AXI27574.1 GI:14134266
KEYWORDS	
SOURCE	
ORGANISM	synthetic construct.
REFERENCE	artificial sequence.
AUTHORS	Xu,W., Lofton-Day,C.E., Henne,R., Yao,Y., Novak,J.E., Foster,D.C.
TITLE	Umbr Polypeptides
DEFINITION	Umbr Polypeptides
ACCESSION	WO 0130850-A 39 03-MAY-2001;
VERSION	
KEYWORDS	
SOURCE	ZymoGenetics, Inc. (US)
FEATURES	Location/Qualifiers
source	1. .519
misc_feature	/organism="synthetic construct" /db_xref="taxon;32630"
misc_feature	/note="degenerate polynucleotide sequence" 1. .519 /note="A,T,C or G" /note="n = A,T,C or G"
BASE COUNT	81 a 65 c 99 g 59 t 215 others
ORIGIN	
Query Match	45.5%; Score 315.4; DB 6; Length 519;
Best Local Similarity	60.9%; Pred. No. 7.3e-81;
Matches	260; Conservative 95; Mismatches 72; Indels 0; Gaps 0;
Qy	1 ATGGATTCGAGAAATTGAGTACTGGACCAATGGGACGGTGTGACCTGGCCAAAGGG 60
Db	1 ATGGATTCGAGAAATTGAGTACTGGACCAATGGGACGGTGTGACCTGGCCAAAGGG 63
Qy	61 TGTGCTCTGACAGGAGCTATCCAAAGGATTCAGGATGGGACGGTGTGACCTGGCCAAAGGG 120
Db	61 TGYGCNCNCGNCARGARTINWSNHBARGATG-TGNTAIGGNGARGGGNGAYCARN 120
Qy	121 TGCACGCTGCCCTCTCGCAGTACAAAGCAGCTGGGGCACCCACAATGTAGAGTG 180

Db 121 TGYACNGCNCNTGCCCCNCNCNMGNMNTAYAARWSNSNTGGGNCAVCAYARTGCARWSN 180
 Qy 181 TGCCTCACCGTGTGCTCATCACATGTTGAGGGTCACTSCACAGCTACTCTTAAT 240
 Db 181 TGYATHACNPTGCGTGTGCGTGTGTCAGTGAGTGTGAGTGTGAGTGTGAGTGTG 240
 Qy 241 GCTGTCCTGIGGGACTGTGTCAGGCCAGGTCTACCGAAAGAACACCCATTGGGGCTGCG 300
 Db 241 GCNGNTGTYGGNGATGTYINCCNGNTYTAWGNARACNGNATHGGNNGYTNCA 300
 Qy 301 GACCAGAGGTGCACTCCGGTGCACAGAGCACCCACCTGTGAGGTCACTGCGCTC 360
 301 GAYCARGARGTGYATHCCNTGYACTHARCARACACNCCNACNWNSNARGTNGARTGCGNTY 360
 Qy 361 CAGTGGAGCTAGTGAGGAGATGACCCAGAGTGGCCCTCTGGAGGSCACCTGTGTT 420
 Db 361 CARYTNTWSNTGNTGARGCNGAYGCNCNCNACNGTNCNCNCAKGARGCNAHYNTG 420
 Qy 421 GCACTCG 427
 Db 421 GCNYTNG 427

RESULT 10

AX127568
 LOCUS AX127568 Sequence 528 bp from Patent WO0130850. DNA linear PAT 15-MAY-2001
 DEFINITION AX127568 ACCESSION AX127568 VERSION AX127568.1
 KEYWORDS SOURCE human.
 ORGANISM Homo sapiens
 REFERENCES 1. (bases 1 to 528)
 AUTHORS Xu,W., Lofton-Day,C.E., Heine,R., Yao,Y., Novak,J.E., Foster,D.C.
 and Yee,D.P.
 TITLE Unir Polypeptides
 JOURNAL Patent: WO 0130850-A 31 03-MAY-2001;
 ZymoGenetics, Inc. (US)
 FEATURES Location/Qualifiers
 source 1. misc_feature
 /organism="Homo sapiens"
 1. .529
 /db:xref="taxon:9606"
 1. .529
 misc_feature
 /note="n = A,T,C or G"
 BASE COUNT 116 a 135 c 126 g 107 t 45 others
 ORIGIN

	Query Match	Score	DB	Length
Best Local Similarity	31.8%	220	4	529
Matches	240	86.0%	Pred.	No. 3.5e-53;
Conservative	16	Mismatches	21	
Indels	2	Gaps	2	

Qy 335 CCACCTCTGGGTCAATGNGCCCTTGCASTGTGAGCTTAGGGAGGCGAGATGCCACAG 394
 Db 6 CNATNNCTGAGGNIGNATGCGNTONAGTINWGSTKAGTGGAGGCGAGATGCCACAG 65
 Qy 395 TGCC-CCTAGGGGCCAACACTTGCTGACTGGAGGAGGCCGCTAGTGGTTAAC 453
 Db 66 TGCCGCTCTGGGCTCTCTCTACTGCAGCACTGTTGCTGAGCTTGCTGAGCTTGCTC 125
 Qy 454 CTGGCCTCTGGGCTCTCTCTACTGCAGCACTGTTGCTGAGCTTGCTGAGCTTGCTC 513
 Db 126 CTGGCCTCTGGGCTCTCTCTGAGCTTGCTGAGCTTGCTGAGCTTGCTGAGCTTGCTC 185
 Qy 514 C-GTGGAGGTGTCAGTCAGCTTGCTGAGCTTGAGGTGATAAACAGCAAGAGGAATCTCTTCCC 572
 Db 186 CSGNGGAGTTGCTGCAAGTGTGAGCTGAGCTGATRAACGCAAGAGGAATCTSTMMTYC 245
 Qy 573 CGTGCACCCAGCAAGGAGCCASTGCTGTGTCAGT 611
 Db 246 CGTGCACCCAGCAAGGAGCCAGTGCTGAGTCCAAAGT 284

RESULT 11

AX127566
 LOCUS AX127566 Sequence 31 from Patent WO0130850. DNA linear PAT 15-MAY-2001
 DEFINITION AX127566 ACCESSION AX127566 VERSION AX127566.1 GI:14134262
 KEYWORDS SOURCE human.
 ORGANISM Homo sapiens
 REFERENCES 1. (bases 1 to 528)
 AUTHORS Xu,W., Lofton-Day,C.E., Heine,R., Yao,Y., Novak,J.E., Foster,D.C.
 and Yee,D.P.
 TITLE Unir Polypeptides
 JOURNAL Patent: WO 0130850-A 31 03-MAY-2001;
 ZymoGenetics, Inc. (US)
 FEATURES Location/Qualifiers
 source 1. misc_feature
 /organism="Homo sapiens"
 1. .529
 /db:xref="taxon:9606"
 1. .529
 misc_feature
 /note="n = A,T,C or G"
 BASE COUNT 116 a 135 c 126 g 107 t 45 others
 ORIGIN

	Query Match	Score	DB	Length
Best Local Similarity	31.8%	220	4	529
Matches	240	86.0%	Pred.	No. 3.5e-53;
Conservative	16	Mismatches	21	
Indels	2	Gaps	2	

Qy 339 CTCTCAGGTCAATGNGCCCTTGACTTGAGGAGATGACCCACAGTGC 398
 Db 1 CTCTCAGGTCAATGNGCCCTTGACTTGAGGAGATGACCCACAGTGC 60
 Qy 399 CCCTCAGGAGGCCAACCTGTGCTGAGGCCAGCCCTGCTAGTGTGTTACCTGGC 458
 Db 61 CCCTCAGGAGGCCAACCTGTGCTGAGGCCAGCCCTGCTAGTGTGTTACCTGGC 120
 Qy 459 CTTCCTGGGGCTCTCTCCCTACTGCAACAGCAACAGACATGCCACGGT-- 516
 Db 121 CTTCCTGGGGCTCTCTCCCTACTGCAACAGCAACATGCCACGGT 180
 Qy 517 -->GAGGTTGCTGCACTGTGAGGCTGATAAACAGCAAGGAGGAATCTCTTCCC 572
 Db 181 TGCAGGAGGTGCTGCACTGTGAGGCTGATAAACAGCAAGGAGGAATCTCTTCCC 240
 Qy 573 CGTGCACCCAGCAAGGAGCCAGGAGCACTGCTGAGCTGTCAGT 611
 Db 241 CGTGCACCCAGCAAGGAGCACTGCTGAGCTGTCAGT 279

COMMENT

RESULTS 11

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission

requests: clonerquest@sanger.ac.uk
 On Mar 12, 2001 this sequence version replaced gi:13121368.

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TRIMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/projects/C.elegans/wormpep>

This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/ChX>

RPI1-133K18 is from the library RPI1-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6

This sequence is the entire insert of clone RPI1-133K18. The true left end of clone RP3-43304 is at 146164 in this sequence.

<pre> 1. . 192505 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="X" /clone "RPI1-133K18" /clone_lbb="RPI1-11.1" feature 2. . 590 /note="match: GSS: Em:AO415618" 8. . 241 /note="LIM4 repeat: matches 4301. . 4547 of consensus" feature 9. . 465 /note="match: GSS: Em:AZ216005" 312. . 748 /note="LIMA2 repeat: matches 5844. . 6304 of consensus" 864. . 1886 /note="LIPALL repeat: matches 4308. . 6165 of consensus" complement((2058..2337) /note="match: GSS: Em:AQ076345" complement((5857..6295) /note="match: GSS: Em:AO456867" region 6871..6916 /note="23 copies 2 mer at 100% conserved" 6947. . 7069 /note="MIR21A repeat: matches 822. . 927 of consensus" 7070..7365 /note="ALU5X repeat: matches 1. . 296 of consensus" 7366..7498 /note="MIR21A repeat: matches 684. . 822 of consensus" 7501..7661 /note="MIR21B repeat: matches 363. . 523 of consensus" 7520..7927 /note="match: GSS: Em:AO021529" 7862..8255 /note="MIR21A repeat: matches 3. . 406 of consensus" 8256..10065 /note="LIM1 repeat: matches -1213. . 643 of consensus" 10066..11582 /note="LIM1 repeat: matches 895. . 2792 of consensus" 11574..12253 /note="LIMA3 repeat: matches 4976. . 5978 of consensus" 12258..13476 /note="LIP15 repeat: matches 5171. . 6055 of consensus" 13477..14163 /note="LIMA1 repeat: matches 5616. . 6299 of consensus" 14164..18546 /note="LIP15 repeat: matches 656. . 5171 of consensus" 19058..19370 /note="LIP13 repeat: matches -651. . -339 of consensus" </pre>	<p>Location/Qualifiers</p>
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repeat_region 19380. 19427
repeat_region /note="LIPAA3 repeat: matches 6109. .6156 of consensus"
repeat_region 20158. 20170
repeat_region /note="L2 repeat: matches 992. .1002 of consensus"
repeat_region 20171. .20593
repeat_region /note="NSTB repeat: matches 1. .426 of consensus"
repeat_region 20594. .20722
repeat_region /note="L2 repeat: matches 1002. .1147 of consensus"
repeat_region 20803. .21457
repeat_region /note="L2 repeat: matches 992. .1002 of consensus"
repeat_region 21924. .22023
repeat_region /note="MTR repeat: matches 1. .426 of consensus"
repeat_region 23030. .23050
repeat_region /note="LIP4 repeat: matches 4. .106 of consensus"
repeat_region 23600
repeat_region /note="LIPB1 repeat: matches 5391 of consensus"
repeat_region 23601. .24341
repeat_region /note="LIP4 repeat: matches 1635. .2587 of consensus"
repeat_region 24558
repeat_region /note="LIPB1 repeat: matches 5596. .6156 of consensus"
repeat_region 24712. .24558
repeat_region /note="LIP4 repeat: matches 4790. .5372 of consensus"
repeat_region 25192
repeat_region /note="match: GSS: Em:AQ617974"
repeat_region 25192
repeat_region /note="LIPB1 repeat: matches 4389. .6155 of consensus"
repeat_region 27175. .28098
repeat_region /note="LIPB1 repeat: matches 3245. .4193 of consensus"
repeat_region 28098. .28541
repeat_region /note="L1 repeat: matches 2176. .2620 of consensus"
repeat_region 28544. .29065
repeat_region /note="LIPAA repeat: matches 5626. .6146 of consensus"
repeat_region 29866. .29291
repeat_region /note="LIPB1 repeat: matches 5398. .5626 of consensus"
repeat_region 29811. .29770
repeat_region /note="LIM2 repeat: matches 1623. .2196 of consensus"
repeat_region 30714. .33390
repeat_region /note="Alusgkx repeat: matches 134. .305 of consensus"
repeat_region 32877
repeat_region /note="LIPB1 repeat: matches 2930. .5805 of consensus"
repeat_region 32882. .33020
repeat_region /note="L2 copies 2 mer ta 66% conserved"
repeat_region 33020
repeat_region /note="LIPB1 repeat: matches 5781. .6155 of consensus"
repeat_region 33538. .35294
repeat_region /note="LIM3a repeat: matches 501. .1804 of consensus"
repeat_region 35271. .35571
repeat_region /note="LIM3a repeat: matches 745. .904 of consensus"
repeat_region 35718. .36216
repeat_region /note="LIM3a repeat: matches 213. .655 of consensus"
repeat_region 36387. .36471
repeat_region /note="MIR repeat: matches 57. .251 of consensus"
repeat_region 36769. .37123
repeat_region /note="LIME1 repeat: matches 5597. .5884 of consensus"
repeat_region 37148. .38332
repeat_region /note="LIMA3 repeat: matches 5105. .6299 of consensus"
repeat_region 38339. .38440
repeat_region /note="L1 repeat: matches 2434. .2535 of consensus"
repeat_region 38446. .38807
repeat_region /note="MIT2B repeat: matches 1. .374 of consensus"
repeat_region 38879. .39795
repeat_region /note="LIMA3 repeat: matches 1. .916 of consensus"
repeat_region 39795. .40402
repeat_region /note="LIP2 repeat: matches 5050. .5656 of consensus"
repeat_region 4003. .40850
repeat_region /note="LIPAA repeat: matches 5699. .6146 of consensus"
repeat_region 40566. .45577
repeat_region /note="HERVL repeat: matches 905. .5578 of consensus"
repeat_region 45578. .45888
repeat_region /note="AlusX repeat: matches 1. .311 of consensus"
repeat_region 45889. .45965
repeat_region /note="HERVL repeat: matches 5578. .5654 of consensus"
repeat_region 46346
repeat_region /note="MLT2B repeat: matches 1. .392 of consensus"
repeat_region 46451. .45981
repeat_region /note="LIM1 repeat: matches -1390. .2500 of consensus"
repeat_region 49288. .50810

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repeat_region /note="LIM4 repeat: matches 3343. .4258 of consensus"
repeat_region 50989. .51126
repeat_region /note="69 copies 2 mer tt 59% conserved"
repeat_region 51129. .51365
repeat_region /note=LIP2 repeat: matches 4727. .5487. of consensus"
repeat_region 52758. .52126
repeat_region /note="L1 repeat: matches 5910. .6146 of consensus"
repeat_region 53994. .54310
repeat_region /note=LIMC5 repeat: matches 7581. .7917 of consensus"
repeat_region 54357. .54551
repeat_region /note="LIP3 repeat: matches 5847. .6127 of consensus"
repeat_region 54560. .54862
repeat_region /note="AluY repeat: matches 1. .303 of consensus"
repeat_region 55116. .57271
repeat_region /note=LIPAB repeat: matches 3978. .6163 of consensus"
repeat_region 57272. .57301
repeat_region /note="LIP4 repeat: matches 5338. .5367 of consensus"
repeat_region 57302. .57608
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Qy 86 AGGATTGGTTATGGAGGGTGAGATGCCATCTGACASCGCTTCCTCCGGCAGGT 145
Db 109481 AGGATTGGTTATGGAGGGTGAGATGCCATCTGACACGGCTTGCCTCTCGCAGGT 109422
Qy 146 ACAAAAGAGCTGGGCCACCAAACTCAGAGTTGATCATCACCTGCTGTCATCAATC 205
Db 109421 ACAAAAGAGCTGGGCCACCAAGATGTCAGATTGATCATCACCTGTCATCAATC 109362
Qy 206 GTGTCAGAGGTCAACTCACAGCTTCAATGCTCTGGGGACTGTGTGCCA 265
Db 109361 GTGTCAGAGGTCAACTCACAGCTTCAATGCTCTGGGGACTGTGTGCCA 109302
Qy 266 GGT 268
Db 109301 GGT 109299

RESULT 13
AC023560/C
LOCUS AC023560 205736 bp **DNA** linear HTG 12-MAR-2000
DEFINITION Homo sapiens chromosome 17 clone RP11-85120 map 17, WORKING DRAFT
ACCESSION AC023560
VERSION AC023560.2
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Mammal; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 205736)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 17, clone RP11-85120
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 205736)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

TITLE
JOURNAL
COMMENT

Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavskiy,L., Boukhaliert,B., Brown,A., Burkett,G., Campoliano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M., Fenestor,J., Ferreira,P., Fitzlough,W., Forrest,C., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., GrandPierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Landers,T., Largoque,K., Lebocky,J., Levine,R., Lieu,C., Liu,G., Lock,K., Macdonald,P., Marquis,N., McCarthy,M., McBwan,P., McGurk,A., McKernan,K., McPheevers,R., Meldrin,J., Meneus,L., Mihowa,T., Miranda,C., Mtenga,V., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,T.M., Peterson,K., Pierre,N., Pisani,C., Poliara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talians,J., Testayre,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,J., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission
 Submitted 15 FEB-2000 Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 12, 2000 this sequence version replaced 91.6978256.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www.seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: 16741
 Center clone name: 85.1_20
 ----- Summary Statistics
 Sequencing vector: M13, M7815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 178666 bases at least 040
 Consensus quality: 109040 bases at least 030
 Consensus quality: 197088 bases at least 020
 Insert size: 194000; agarose-fp
 Insert size: 202436; sum-of-contigs
 Quality coverage: 4.2 in Q20 bases; agarose-fp
 Quality coverage: 4.0 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 34 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 1267: contig of 1267 bp in length
 * 1268 1367: gap of 100 bp
 * 1368 2402: contig of 1035 bp in length
 * 2403 2502: gap of 100 bp
 * 2503 3524: contig of 1022 bp in length
 * 3525 3624: gap of 100 bp
 * 3625 4913: contig of 1289 bp in length
 * 4914 5013: gap of 100 bp
 * 5014 6289: contig of 1276 bp in length
 * 6290 6389: gap of 100 bp
 * 6390 7655: contig of 1266 bp in length
 * 7656 7755: gap of 100 bp
 * 7756 9267: contig of 1512 bp in length
 * 9268 9367: gap of 100 bp
 * 9368 11138: contig of 1771 bp in length
 * 11139 11238: gap of 100 bp
 * 11239 13822: contig of 2584 bp in length
 * 13823 13922: gap of 100 bp

FEATURES	2 (bases 1 to 744)	Db	643	TGCAAGAGCAGTTCA	658
AUTHORS	Kojima,T. and Kitamura,T.	RESULT	15	AF167553	AF167553
TITLE	Direct Submission	DEFINITION	Mus musculus TAJ-alpha short mRNA, complete cds.		
JOURNAL	Submitted (23-MAR-2000) Tetsuo Kojima, Chugai Research Institute for Molecular Medicine, Inc., Cytokine Research Program; 153-2 Nagai, Niihari, Ibaraki 300-1101, Japan (E-mail:kojimat@climed.com, Tel:81-298-306211, Fax:81-298-306270)	ACCESSION	AF167553		LINEAR
SOURCE	Location/Qualifiers	VERSION	AF167553.1	G1:8071639	ROD 25-MAY-2000
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BASE COUNT	162 a 208 c 211 g 163 t	ORGANISM	MUS MUSCULUS		
ORIGIN		REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurogathi; Muridae; Murinae; Mus.		
Query Match	23.5%; Score 163.2; DB 10; Length 744;	AUTHORS	Eby,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.		
Best Local Similarity	58.1%; Pred. No. 1.7e-36;	TITLE	TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family, Activates the C-Jun N-terminal Kinase Pathway and Mediates Caspase-Independent Cell Death		
Matches	288; Conservative 0; Mismatches 208; Indels 0; Gaps 0;	JOURNAL	J. Biol. Chem. 275 (20), 15336-15342 (2000)		
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Db	163 GATTCGAGCCGCGAGAACATTCAGGATCTGCTCCAAAGGAATGTCAGTGT 222	REFERENCE	2 (bases 1 to 886)		
Qy	64 GGTCCTGGACAGGAGCTATCCAAGGATGGTTATGGAGGGTGGAGATGCCATCTGC 123	AUTHORS	Chaudhary,P.M.		
Db	223 GGACCTTGGCATGGAGTTGTCGAAGGATGGCTCTGGCATGGAGATGCCAGTGT 282	TITLE	Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical Center, 5233 Harry Hines Blvd., Dallas, TX 75235-8593, USA		
Qy	124 ACAGCCCTGCCCCTCTGGCAGAGTACAAGAGAGCTGGGCTACAGTGT 183	JOURNAL	Location/Qualifiers		
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